

Figure 1

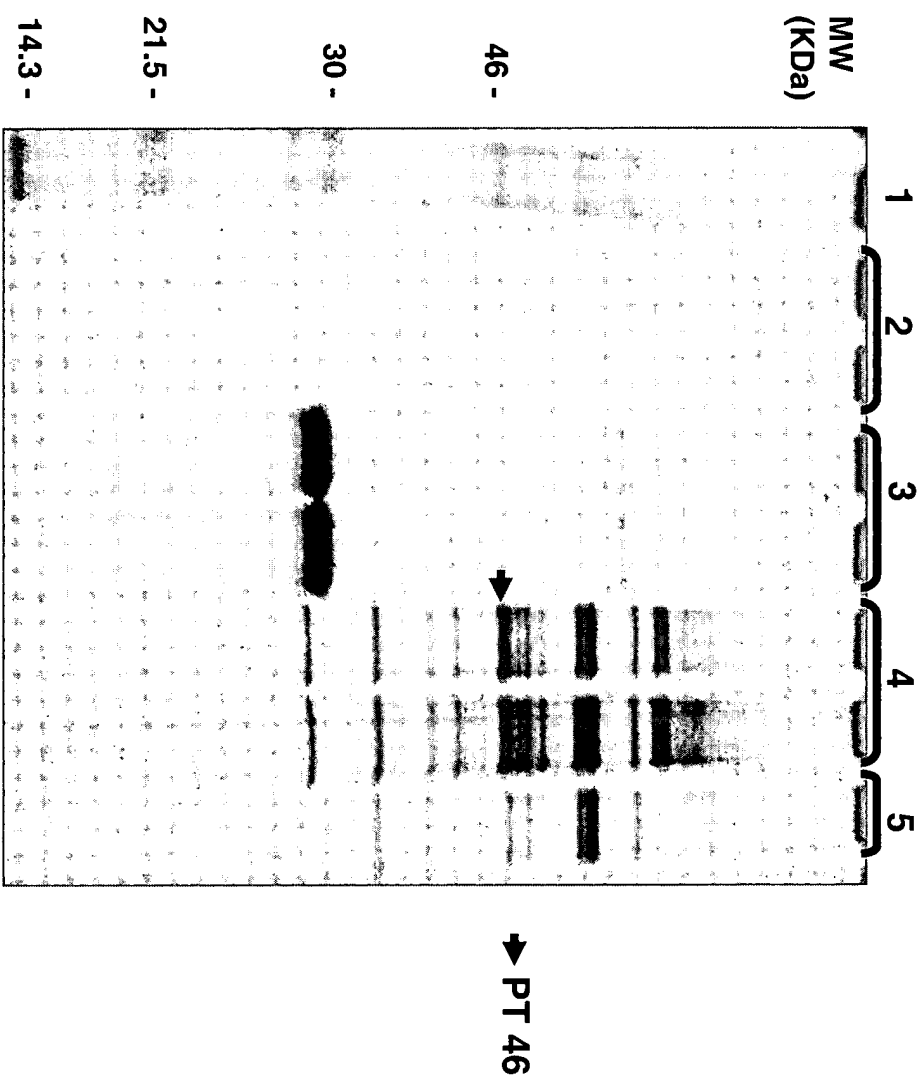


Figure 2

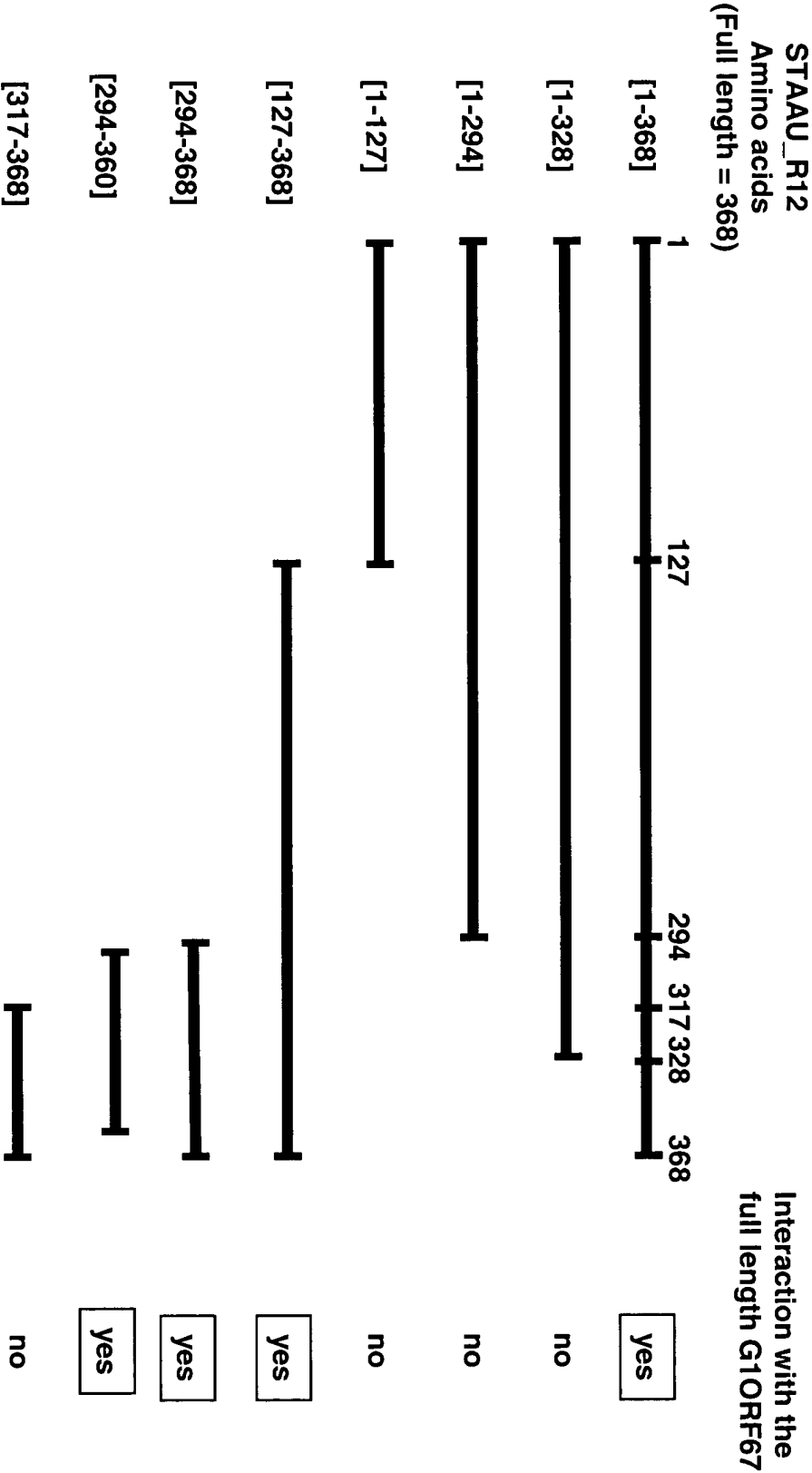


Figure 3A

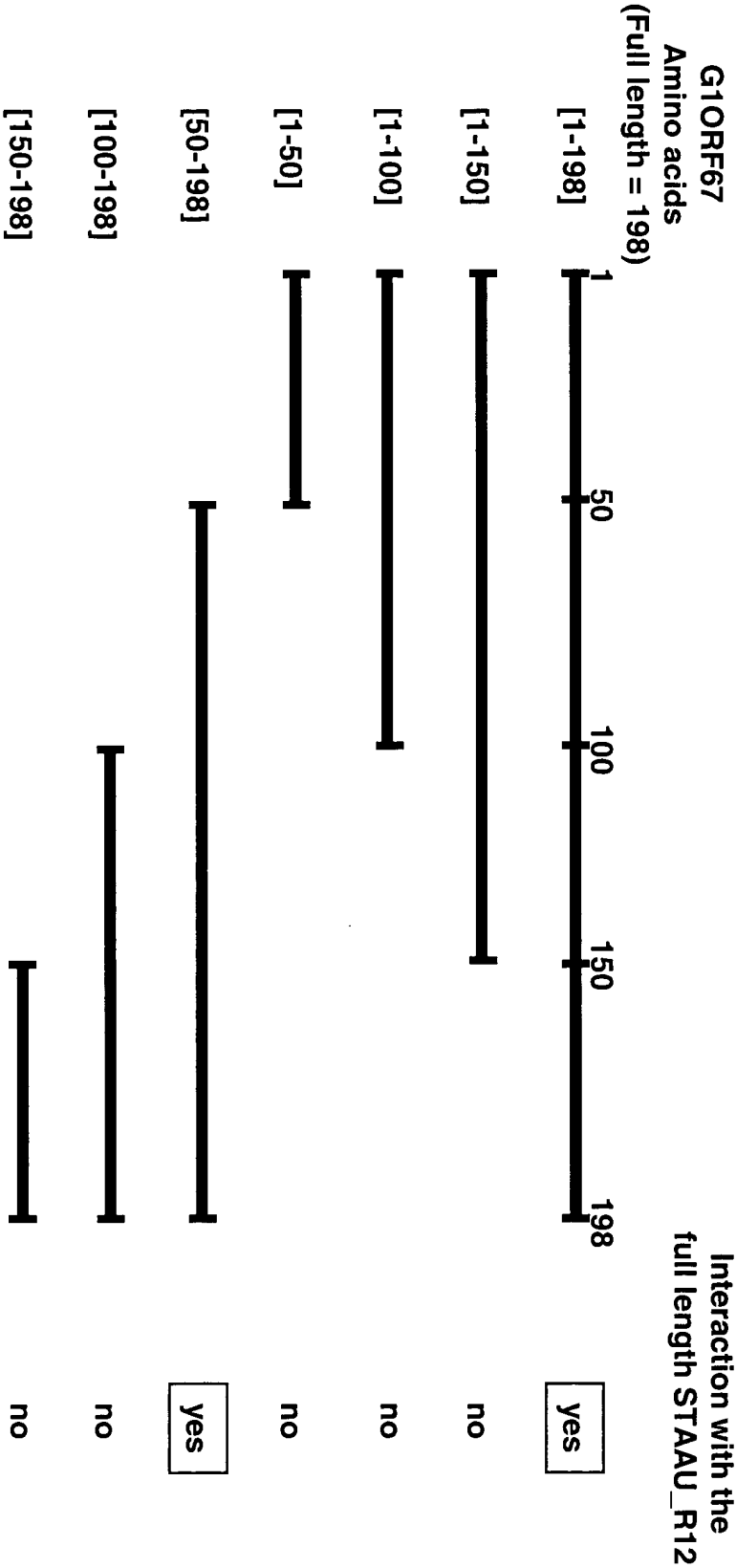


Figure 3B

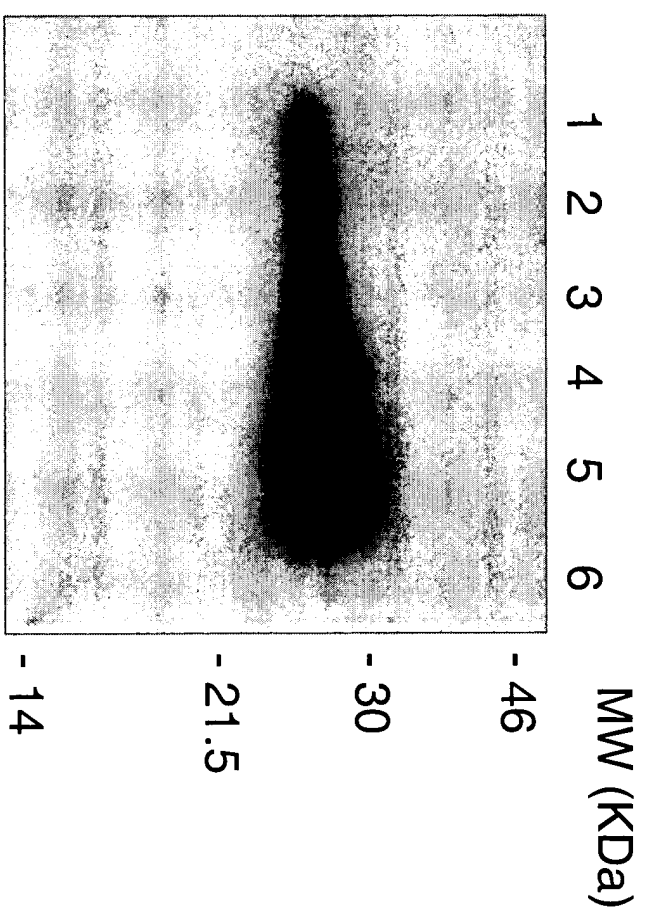


Figure 4

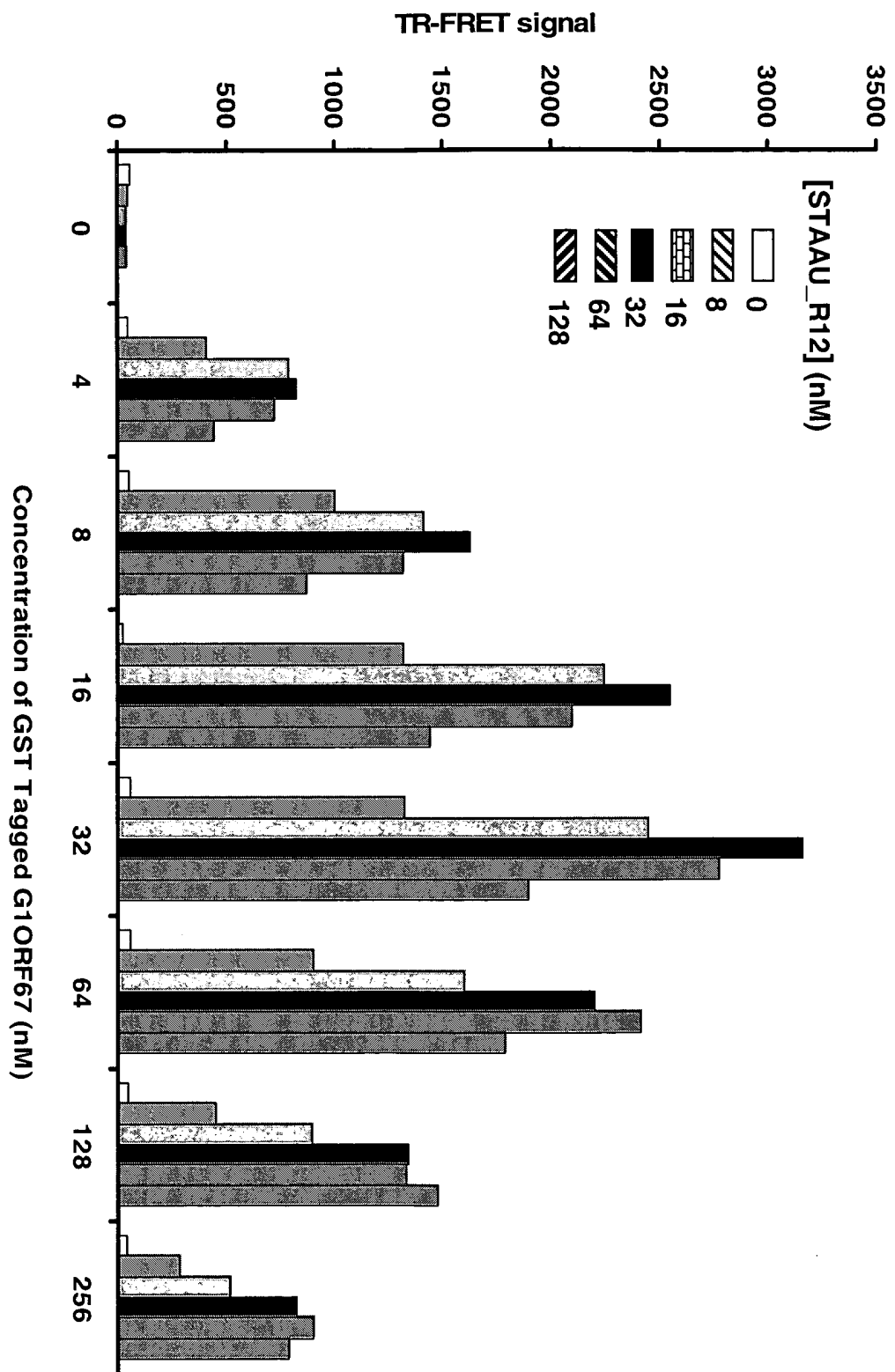


Figure 5A

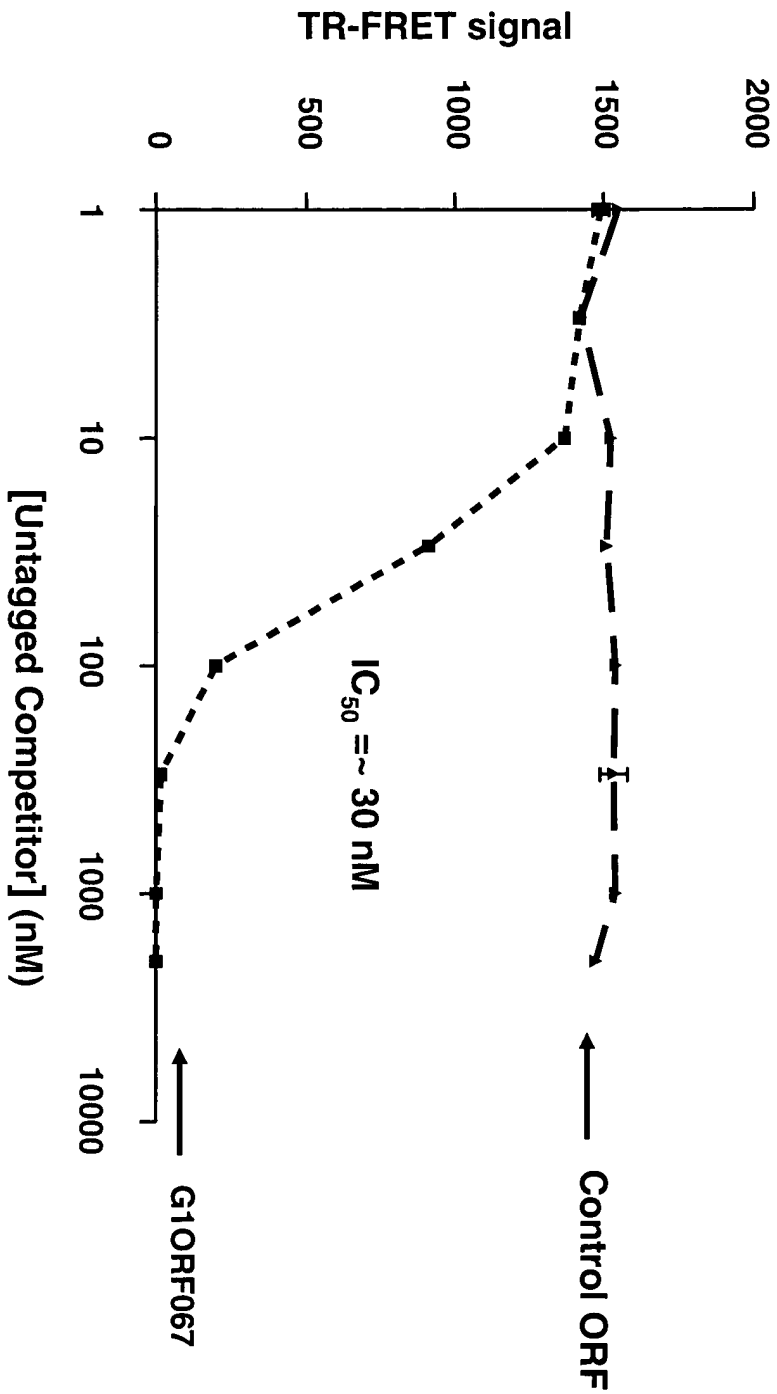


Figure 5B

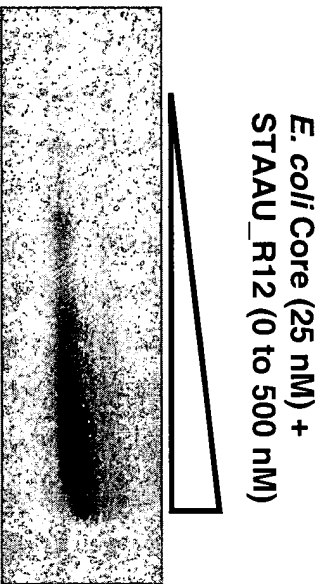


Fig. 6A

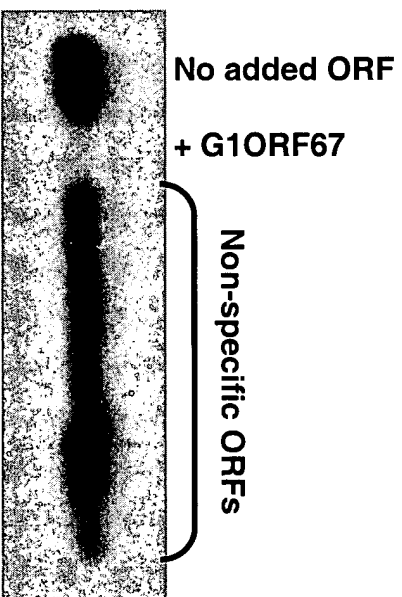


Fig. 6B

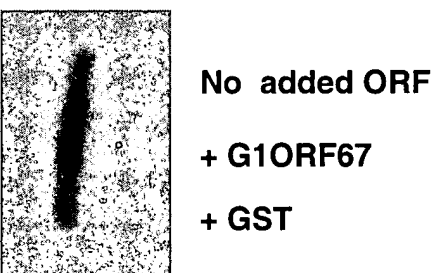


Fig. 6C

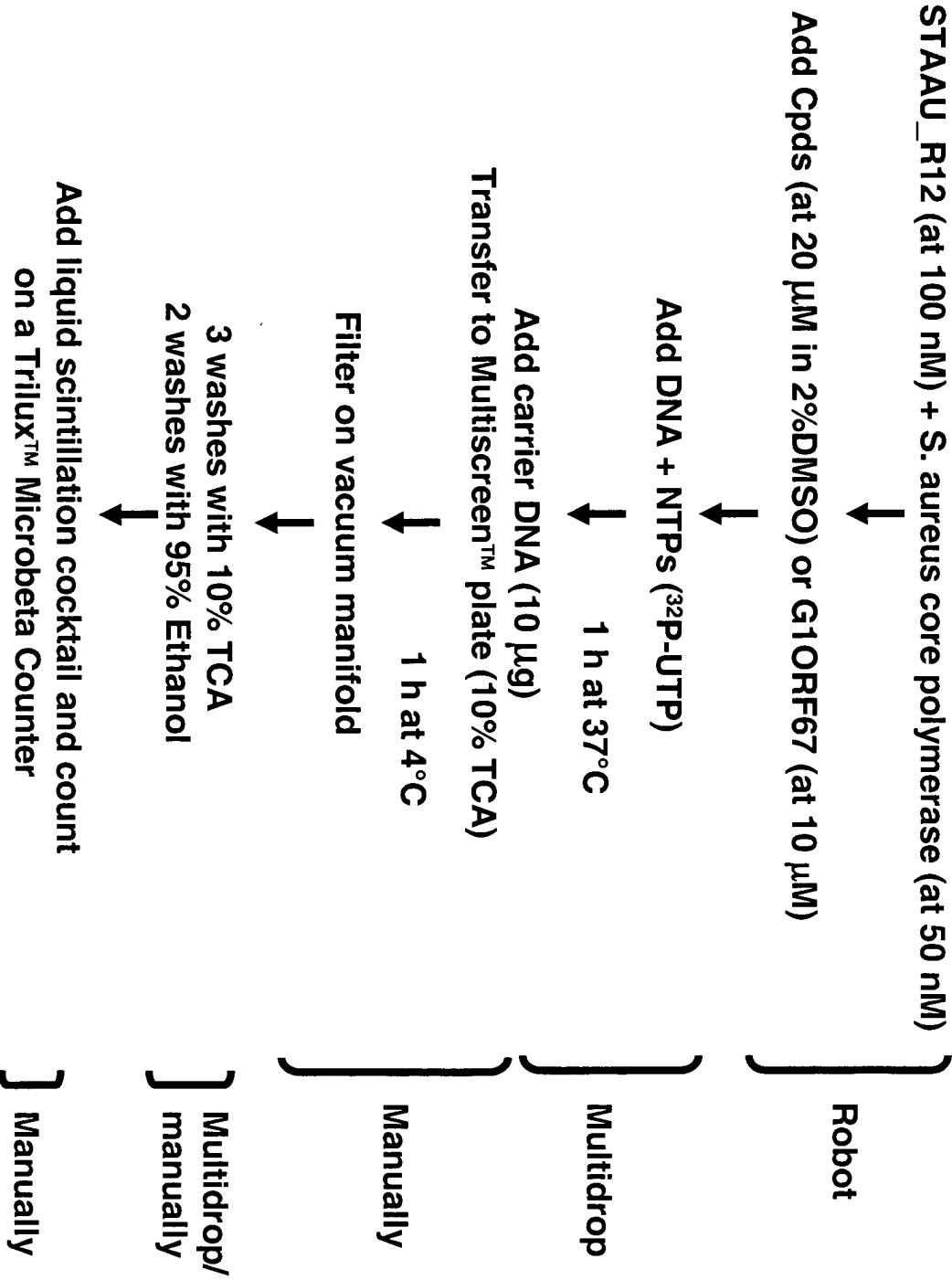


Figure 7

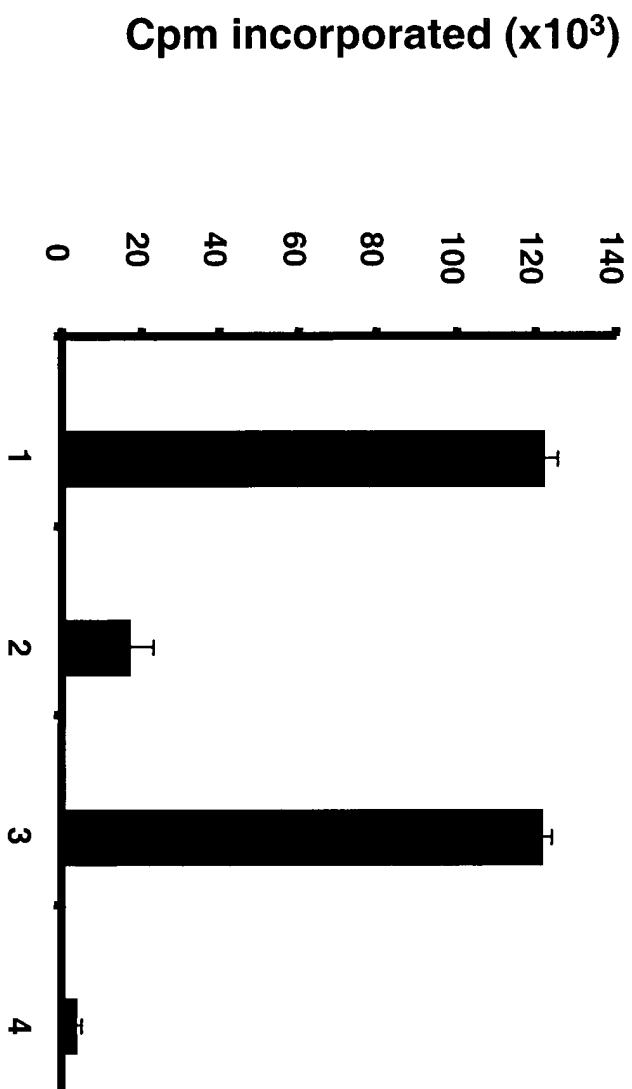
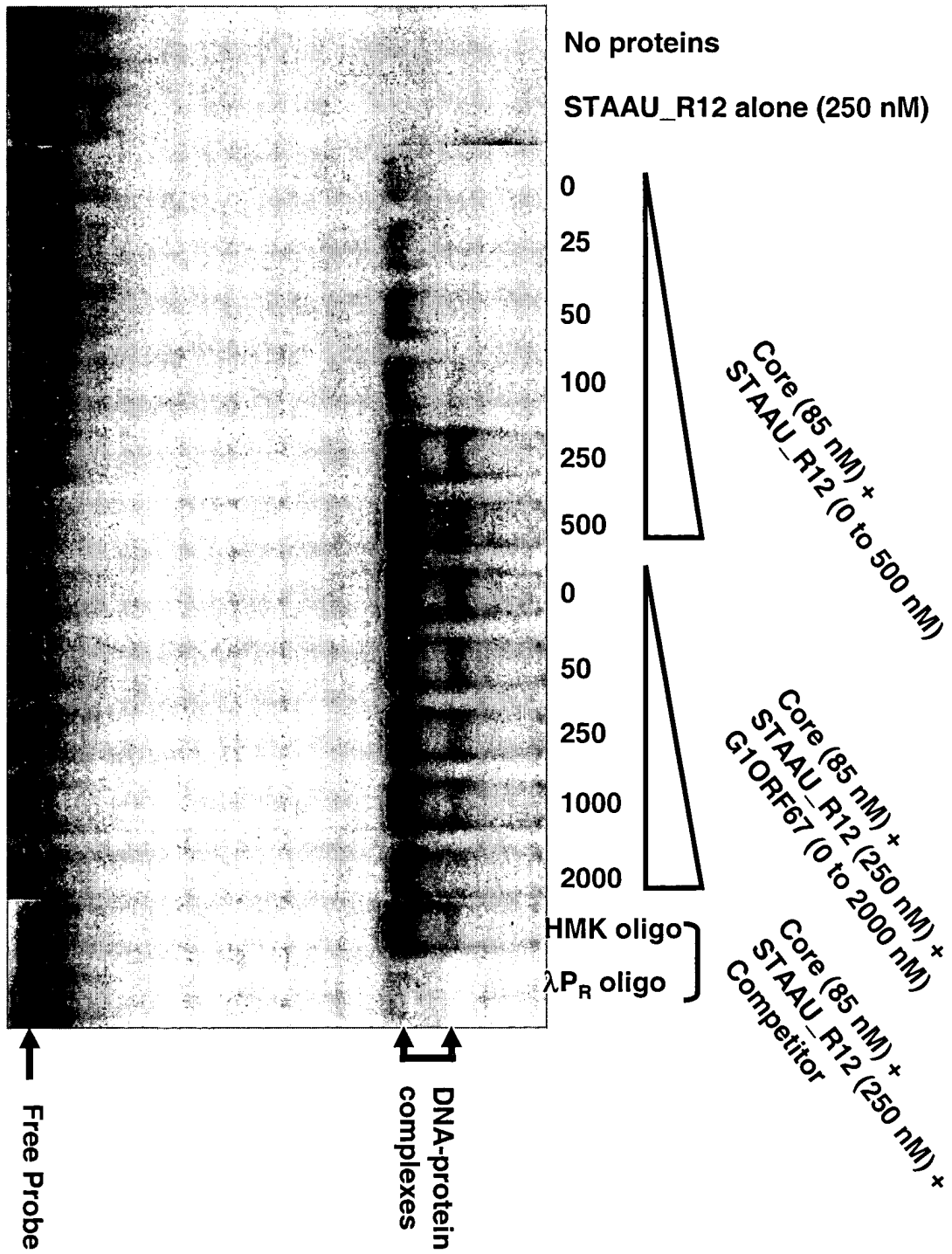


Figure 8

Figure 9



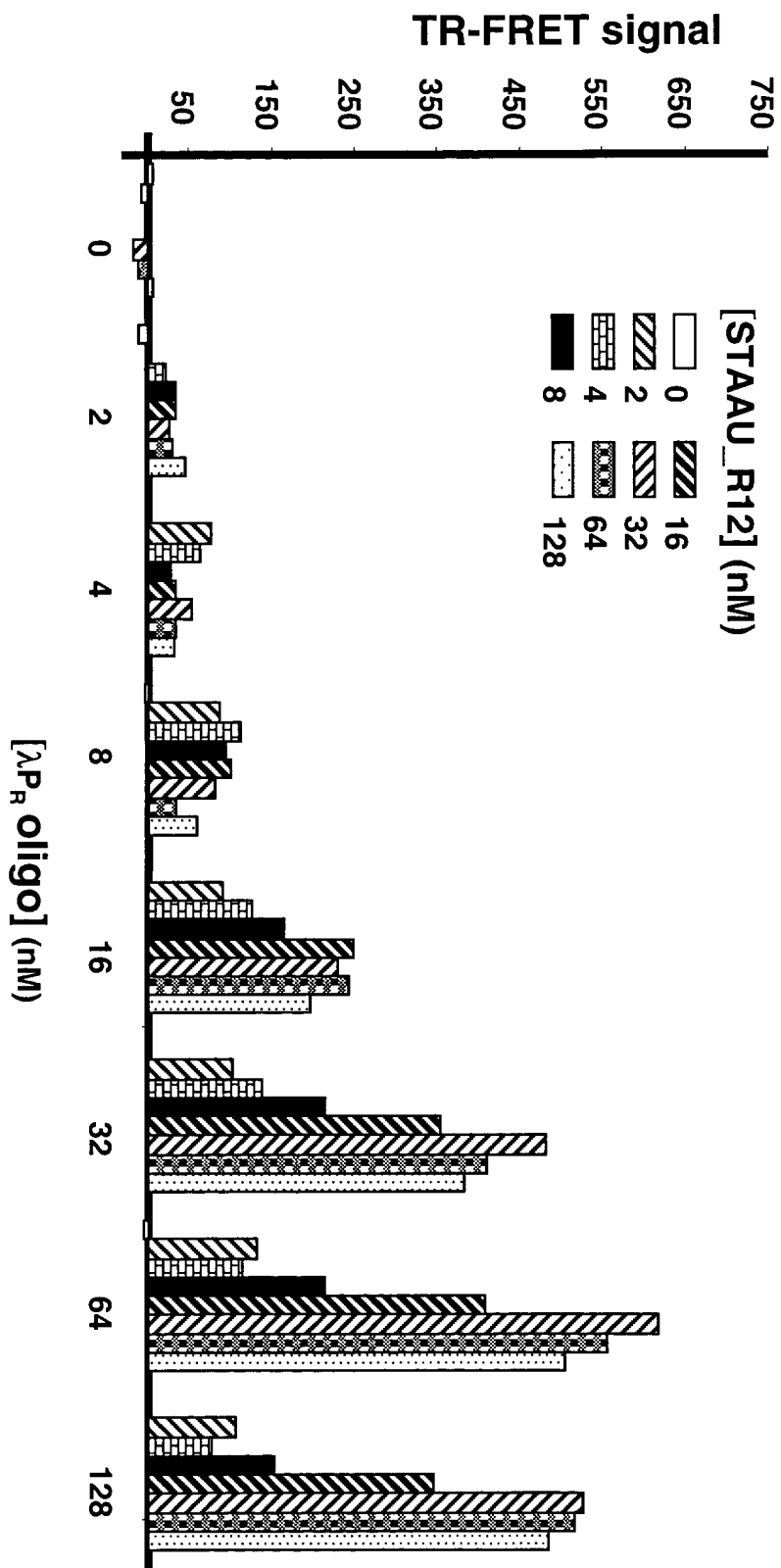


Figure 10

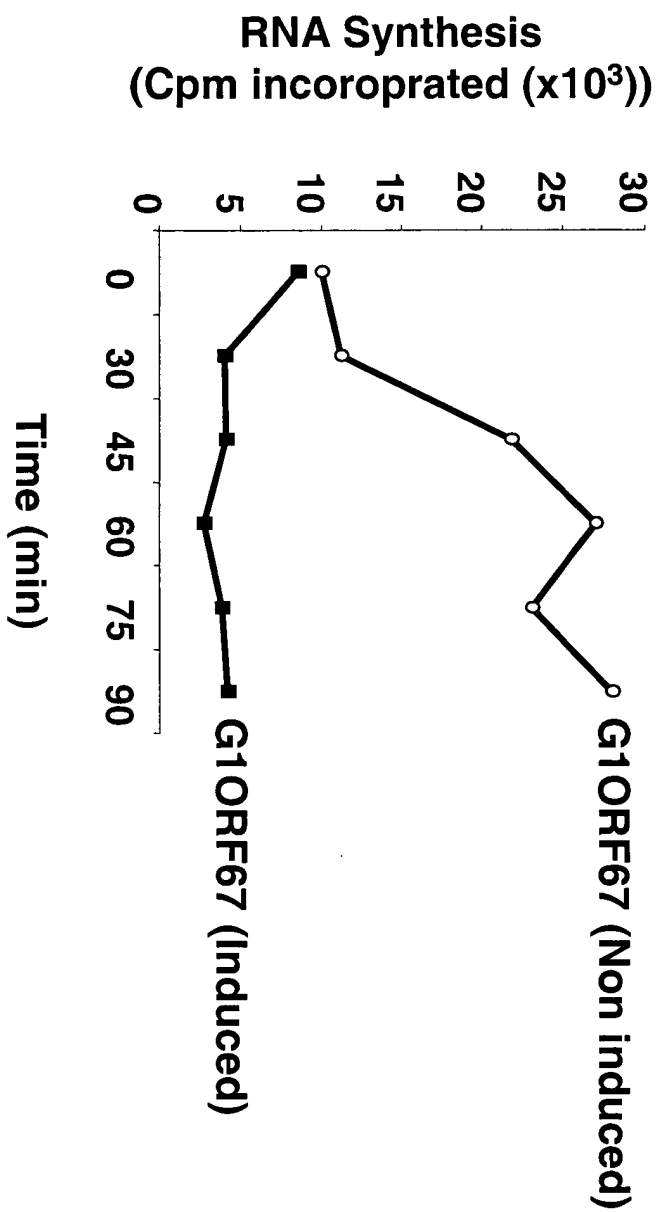


Figure 11

Seq1: G1ORF067 (SEQ ID NO: 7)
Seq2 TwortORF065 (SEQ ID NO: 10)

Substitution matrix: blosum62

Gap penalty: - (11 + 1 * (gap length))

Score: 388

Identical: 87/199 (43%), **Similar:** 124/199 (62%), **Gap:** 5/199 (2%)

```
seq1      1 MKLKILDKDNATLNVFHRNKEHKTIDNVPTANLVDWYPLSNAYEYKLSRNGEYLELKRLR   60
          ||||| :|      | |      |      | :|| :|: :||| |||| | | :   : | |||||
seq2      1 MKLKIKNKFMGVLEV--TNSMGVTKLDVPLSNIHEWYPFSNAYSYKYNVKTCDLVLR   58

seq1     61 STLPSSYGLDDNNQDIIRDNNHRCKIGYWYNPAVRKDNLKIIEKAKQYGLPIITEEYDAN  120
          |:| | |||:: ::: | : |      | | :|: || || ||| |||||:| |||:|
seq2     59 SSLPVSYGIERASKEY--DKDKVCNTVTWINHSVKDSNLHIINKAKSYGLPVITEKYTYE  116

seq1    121 TVEQGFRDIGVIFQSLKTIVVTRYLEGKTEEELRIFNMKSEESQLNEALKESDFSVDLTY  180
          |: || : ||| ||::: |||| | : | : |:| : |:::| :: ||
seq2    117 DVDYGFAQLNVIFSELKSLIINRYLEDKDGSFIVKFKRHNPETQYHLAVQDADEVINNTY  176

seq1    181 SDLGQIYNMLLLMKKISK-      198
          :|||:| |||||:|
seq2    177 DELGQMYKMLLLMKKLSKY      195
```

Figure 12